Amendments To The Specification:

Please replace the paragraph beginning on page 6 and ending on page 7 with the following:

--Fig. 3 shows the binding of the RNA ligand to the GST-RBD protein. Percentage of the binding of the RNA ligand to GST-RBD is based on a value measured by the nitrocellulose filter binding assay. In Fig. 3, a closed circle indicates the use of an RNA of ~~sequence No. 1~~ SEQ ID NO:1, a closed square the use of an RNA of ~~sequence No. 7~~ SEQ ID NO:7, and a closed triangle the use of an RNA of ~~sequence No. 11~~ SEQ ID NO:11.--

Please replace the second full paragraph on page 8 with the following:

--As the nucleic acid molecular seed of the present invention, an RNA containing any one of base sequences, ~~sequence Nos. 1 to 28~~ SEQ ID NOs:1-28, preferably ~~sequence Nos. 1 to 8~~ SEQ ID NOs:1-8 or ~~sequence Nos. 25 to 28~~ SEQ ID NOs:25-28 of the Sequence Listing is mentioned.--

Please replace the paragraph beginning on page 8 and ending on page 9 with the following:

--The RNAs of the present invention shown in the sequence ~~numbers~~ listing have an ability of binding to the "target proteins of Ras". More specifically, the RNAs are characterized in that they are specifically bound to the Ras binding domain (RBD) of Raf-1, and the nucleic acid molecular seed of the present invention is not limited to the base sequences shown in the foregoing ~~sequence Nos. 1 to 28~~ SEQ ID NOs:1-28. A seed having a base sequence in which at least one base of ~~sequence Nos. 1 to 28~~ SEQ ID NOs:1-28 of the Sequence Listing is deleted and substituted with another base and/or another base is added is also available so long as it has an ability of binding to the "target proteins of Ras".--

Please replace the second full paragraph on page 9 with the following:

--These RNAs of the present invention can also be reversely transcribed, as required, into DNAs having complementary base sequences to the RNAs. Accordingly, the present invention relates to nucleic acid molecular seeds such as RNAs, DNAs and the like, containing any one of base sequences of ~~sequence Nos. 1 to 28~~ SEQ ID NOs:1-28 of the Sequence Listing or a base sequence in which at least one base thereof is deleted and substituted with another base and/or at least one base is added.--

Please replace the first full paragraph on page 10 with the following:

--Incidentally, RNAs comprising approximately 60 bases shown in ~~sequence Nos. 29 to 52~~ SEQ ID NOs:29-52 of the Sequence Listing indicate base sequences comprising approximately 60 bases in a central portion of RNAs shown in ~~sequence Nos. 1 to 24~~ SEQ ID NOs:1-24. Further, RNAs comprising approximately 45 bases shown in ~~sequence Nos. 53 and 54~~ SEQ ID NOs:53 and 54 of the Sequence Listing indicate base sequences comprising approximately 45 bases in a central portion of RNAs shown in ~~sequence Nos. 25 to 28~~ SEQ ID NOs:25-28. Moreover, ~~sequence Nos. 55 to 60~~ SEQ ID NOs:55-60 of the Sequence Listing show base sequences of primers used in specific examples of the present invention.--

Please replace the second full paragraph on page 14 with the following:

--The sequences of the total sizes (approximately 100 bases) of the 8 types of RNAs (21.01 to 21.08 in Fig. 2) in group 1 are shown in ~~sequence Nos. 1 to 8~~ SEQ ID NOs:1-8.--

Please replace the third full paragraph on page 14 with the following:

--The interaction between the 10 RNAs among them and GST-RBD was examined by a binding assay using a nitrocellulose filter. The results are shown in the right column of Fig. 2 in terms of RNA binding (%). As a result, the RNAs in group 1 showed the satisfactory binding to GST-RBD, whereas the RNAs in group 2 did not show the satisfactory binding. The Kd values of the RNAs shown in ~~sequence Nos. 1~~ SEQ ID NO:1 (21.01 in Fig. 2) and ~~7~~ SEQ ID NO:7 (21.07 in Fig. 2) were both 300 nM. Meanwhile, that of the RNA in ~~sequence No. 11~~ SEQ ID NO:11 (21.11 in Fig. 2) was a micromol order (refer to Fig. 3). Fig. 3 shows percentages of binding to GST-RBD when using RNAs having ~~sequence Nos. 1~~ SEQ ID NO:1 (closed circle), ~~7~~ SEQ ID NO:7 (closed square) and ~~11~~ SEQ ID NO:11 (closed triangle) at various concentrations (nM).--

Please replace the first full paragraph on page 15 with the following:

--It was then examined whether the RNA aptamers in group 1 inhibit the interaction between Ras and RBD (refer to Fig. 4). The RNAs having ~~sequence Nos. 1~~ SEQ ID NO:1 (A in Fig. 4), ~~7~~ SEQ ID NO:7 (B in Fig. 4), ~~11~~ SEQ ID NO:11 (C in Fig. 4) and ~~12~~ SEQ ID NO:12 (D in Fig. 4) (corresponding to 21.01, 21.07, 21.11 and 21.12 in Fig. 2, respectively) were tested at concentrations of 0 to 12.5 μm. These were incubated with GST-RBD supported on a Sepharose matrix and Ras in GTPγS or GDP. In the presence of the RNAs (lanes 3, 4 and 5 in Fig. 4; lane 3 is 20-pmol RNA, lane 4 200-pmol RNA and lane 5 2,000-pmol RNA) or in the absence of the RNAs (lanes 1 and 3 in Fig. 4; lane 1 was in the presence of GDP and lane 2 in the presence of GTP), the binding between GST-RBD and Ras was examined by immunoblotting with anti-Ras antibody RAS004.--

Please replace the second full paragraph on page 15 with the following:

--In Fig. 4, "Ras" indicates Ras bound to GST-RBD, arid "GST-RBD" indicates as a background that GST-RBD is solely present. As stated carlier, the RNA of ~~sequence No. 12~~ SEQ ID NO:12 (D in Fig. 4) which is scarcely bound to GST-RBD did not inhibit the binding of Ras to GST-RBD even at the concentration of 12.5 μM. This was the same with the RNA of ~~sequence No. 11~~ SEQ ID NO:11 (C in Fig. 4) in which the kd value was a micromol order.--

Please replace the paragraph beginning on page 15 and ending on page 16 with the following:

--On the other hand, the RNAs of ~~sequence Nos. 1~~ SEQ ID NO:1 (A in Fig. 4) and ~~7~~ SEQ ID NO:7 (B in Fig. 4) in group 1 effectively inhibited the interaction between Ras and RBD. The reason is considered to be that these RNAs were bound to RBD. And, the kd value of the GTP binding Ras and RBD of Raf-1 is 18 nM (Hermann, C., et al., J. Biol. Chem., 270, 2901- 2905 (1995)), and the RNAs of ~~sequence Nos. 1 and 7~~ SEQ ID NO:1 and SEQ ID NO:7 have the binding ability which is 10 times lower than that. Despite this, these RNAs inhibit the interaction between Ras and Raf-1.--

Please replace the second full paragraph on page 16 with the following:

--Another in vitro selection was conducted by using a double-stranded DNA pool obtained by synthesizing a single-stranded DNA pool (200 pmols, 1.2×10^{14} molecules) having a sequence of 5'-ggtaa tacga ctcac tatag ggagt ggagg aattc atcga ggcat-3' (SEQ ID NO:59) at the 5'-terminus and 5'-catat gcctt agcga cagca agctt ctgc-3' (SEQ ID NO:60) at the 3'-terminus and containing random 45 bases in the middle thereof and converting this single-stranded DNA pool to the double-stranded DNA pool by PCR.--

Please replace the last six lines on page 16 with the following:

--Consequently, novel RNA atamers to be bound to Raf-1 RBD could be obtained. These sequences are as follows, and shown in ~~sequence Nos. 25 to 28~~ SEQ ID NOs:25-28 of the Sequence Listing.

~~Sequence 25~~ SEQ ID NO:25

gggaguggag gaauucaucg aggcauaugu cgacuccguc uuccuucaaa ccaguuauaa 60
auugguuuua gcauaugccu uagcgacagc aagcuucugc 100--

Please replace the first 23 lines on page 17(the entirety of the page, except for the paragraph beginning on page 17 and ending on page 18) with the following:

--~~Sequence 26~~ SEQ ID NO:26

gggaguggag gaauucaucg aggcaugacc ucccguggca guagggguaa aaauuaucuu 60
ccuacacuuc ucaugccuua gcgacagcaa gcuucugc 98

~~Sequence 27~~ SEQ ID NO:27

gggaguggag gaauucaucg aggcauaugu cgacuccguc uuccuucaaa ccaguuauaa 60
auugguuuua gcauaugccu uagcgacagc 90

~~Sequence 28~~ SEQ ID NO:28

gggaguggag gaauucaucg aggcauaugu cgacuccguc uuccuucaaa ccaguuauaa 60
auugguuuua gcauaugccu 80

The Kd values of the RNAs shown in ~~sequence Nos. 25, 26 and 28~~ SEQ ID NOs:25, 26, and 28 among these RNAs and GST-RBD were as follows.

~~RNA of sequence 25~~ SEQ ID NO:25: 124 nM

~~RNA of sequence 26~~ SEQ ID NO:26: 295 nM

~~RNA of sequence 28~~ SEQ ID NO:28: 176 nM

And, the RNAs of ~~sequences 25 to 28~~ SEQ ID NOs:25-28 all inhibited the binding between Ras and Raf-1 RBD depending on the amounts.

~~Sequence Nos. 25, 27 and 28~~ SEQ ID NOs:25, 27, and 28 are different in the size of the 3'-terminus. From this fact, it is presumed that the RNAs of 99 to 81 bases (90 bases correspond to ~~sequence 27~~ SEQ ID NO:27) up to ~~sequence 28~~ SEQ ID NO:28 through the decrease by each one base from the 3'-side of ~~sequence 25~~ SEQ ID NO:25 also have the activity.

Sequences of 45 bases corresponding to the random region were shown in ~~sequence Nos. 53 and 54~~ SEQ ID NOs:53 and 54.--

Please replace the paragraph beginning on page 17 and ending on page 18 with the following:

--The RNA aptamers of ~~sequences 25 to 28~~ SEQ ID NOs:25-28 obtained here can be provided through transcription from synthetic DNAs or through synthesis.--

Please replace the first full paragraph on page 25 with the following:

--Selection of RNAs bound to Raf-1 RBD from the first RNA pool in Example 6, reverse transcription of RNAs to DNAs, amplification and transcription of DNAs to RNAs were repeated 10 times to obtain RNAs of sequence Nos. 25 and 26 of the Sequence Listing.--

Please replace the heading located after the first full paragraph on page 25 with the following:

--Example 8 (RNAs of ~~sequence Nos. 27 and 28~~ SEQ ID NOs:27 and 28)--

Please replace the second full paragraph on page 25 (under the Example 8 heading) with the following:

--DNAs which had a complementary sequence of an RNA of ~~sequence no. 25~~ SEQ ID NO:25 and of which the 3-terminus side was shortened were obtained by PCR using a primer 5'-ggtaa tacga ctcac tatag ggagt ggagg aattc atcg-3' (SEQ ID NO:63) and a primer 5'-gctgt cgcta aggca tatgc taaaa c-3' (SEQ ID NO:65) or 5'-aggca tatgc taaaa ccaat ttata ac-3' (SEQ ID NO:66). From these DNAs, RNAs of ~~sequence Nos. 27 and 28~~ SEQ ID NOs:27 and 28 of the Sequence Listing were obtained.--

Please replace the second full paragraph on page 26 with the following:

--In the RNAs of ~~sequence Nos. 25 to 28~~ SEQ ID NOs:25-28, the decrease in the amount of Ras was observed according to the RNA amount.--